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1 CGGTGGCGCCCGTTCTAGAACTAGTGGATCCCCCGGGATGCAGGAATTCGGCACGAGAAA 60
61 GTGCGGCGGAAAGTAAGAGGCTCACTGGGGAAGACTGCCGGGATCCAGGTCTCCGGGGTC 120
121 CGCTTTGGCCAGAGGCGCGGAAGGAAGCAGTGCCCGGGCAGACTGCACCCATCCCGGCTG 180
181 CTJTTGCTGCGCCCTCTCAGCTTCCCAAGAAAGGCATCGTCATGTGATCATCACCTAAGA 240
241 ACTAGAACATCAGCAGGCCCTTAGAAGCCTCACTCTTGCCCTCCCTTTAATATCTCAAA 300
301 GGATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAGTGATG 360
 M T L L W C V V S L Y F Y G I L Q S D A
361 CCTCAGAACGCTGCGATGACTGGGGAAGTAGACACCATGAGGCAAATCCAAGTGTTTGAAG 420
 S E R C D D W G L D T M R Q I Q V F E D
421 ATGAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCA 480
 E P A R I K C P L F E H F L K F N Y S T
481 CAGCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAAGCAGGACCGGGACCTTG 540
 A H S A G L T L I W Y W T K Q D R D L E
541 AGGAGCCAATTAACCTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGT 600
 E P I N F R L P E N R I S K E K D V L W
601 GGTTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTA 660
 F R P T L L N D T G N Y T C M L R N T T
661 CATATTGCAGCAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATT 720
 Y C S K V A F P L E V V Q K D S C F N S
721 CCCCCATGAACTCCCAGTGCATAAACTGTATATAGAATATGGCATTGAGGATCACTT 780
 P M K L P V H K L Y I E Y G I Q R I T C
781 GTCCAAATGTAGATGGATATTTTCCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGG 840
 P N V D G Y F P S S V K P T I T W Y M G
841 GCTGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCC 900
 C Y K I Q N F N N V I P E G M N L S F L
901 TCATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATG 960
 I A L I S N N G N Y T C V V T Y P E N G
961 GACGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATG 1020
 R T F H L T R T L T V K V V G S P K N A
1021 CAGTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCAGGAG 1080
 V P P V I H S P N D H V V Y E K E P G E
1081 AGGAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGG 1140
 E L L I P C T V Y F S F L M D S R N E V
1141 TTTGGTGGACCATTGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACG 1200
 W W T I D G K K P D D I T I D V T I N E
1201 AAAGTATAAGTCATAGTAGAACAGAAGATGAACTAGAACTCAGATTTTGAGCATCAAGA 1260
 S I S H S R T E D E T R T Q I L S I K K
1261 AAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCG 1320
 V T S E D L K R S Y V C H A R S A K G E
1321 AAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAGGTAATAGATGCGGTGAGTGATGAATCT 1380
 V A K A A K V K Q K G N R C G Q *

FIG.1A

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1381	CTCAGCTCCAAATTAACATTGTGGTGAATAAGGACAAAAGGAGAGATTGAGAACAAGAGA	1440
1441	GCTCCAGCACCTAGCCTGACGGCATCTAACCCATAGTAATGAATCAAACCTTAAATGAAAA	1500
1501	ATATGAAAGTTTTTCATCTATGTAAGATACTCAAAATATTGTTTCTGATATTGTTAGTACC	1560
1561	GTAATGCCCAAATGTAGCTAAAAAATCGACGTGAGTACAGTGAGACACAATTTTGTGTC	1620
1621	TGTACAATTATGAAAAATTA AAAACAAAGAAAATATTCAAAGCTACCAAAGATAGAAAAA	1680
1681	ACTGGTAGAGCCACATATTGTTGGTGAATTATTAAGACCCTTTTAAAAATCATT CATGGT	1740
1741	AGAGTTTAAGAGTCATAAAAAAGATTGCATCATCTGACCTAAGACTTTTCGGAATTTTCC	1800
1801	TGAACAAATAACAGAAAGGGAATTATATACCTTTTAAATATTATTAGAAGCATTATCTGTA	1860
1861	GTTGTAAACATTATTAATAGCAGCCATCCAATTGTATGCAACTAATTAAGGTATTGAAT	1920
1921	GTTTATTTTCCAAAAATGCATAATTATAATATTATTTTAAACACTATGTATCAATATTTA	1980
1981	AGCAGGTTTATAATATACCAGCAGCCACAATTGCTAAAATGAAAATCATTTAAATTATGA	2040
2041	TTTTAAATGGTATACACATGATTTCTATGTTGATAGTACTATATTATTCTACAATAAATG	2100
2101	GAAATTATAAAGCCTTCTTGTCAGAAAGTGCTGCTCCTAAAAAAAAAAAAAAAAAAAAA	2155

FIG. 1B

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Query:	303	MTLLWCVSLYFYGILQSDASERCDDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYS	482
		M LLW ++SL FYGILQS ASERDDWGLDTRMQIQVFEDEPARIKCPLFEHFLK+NYST	
Sbjct:	1	MGLLWYLMSLSFYGILQSHASERCDDWGLDTRMQIQVFEDEPARIKCPLFEHFLKYNYS	60
Query:	483	AHSAGLTLIWYTKQDRDLEEPINFRLPENRISKEKDVLFWRPTLLNDTGNVTCMLRNTT	662
		AHS+GLTLIWYWT+QDRDLEEPINFRLPENRISKEKDVLFWRPTLLNDTGNVTCMLRNTT	
Sbjct:	61	AHSSGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLFWRPTLLNDTGNVTCMLRNTT	120
Query:	663	YCSKVAFPLEVVQKDSFCNSPMKLPVHKL YIEYGIQRITCPNVDGYFPSSVKPTITWYMG	842
		YCSKVAFPLEVVQKDSFCNS M+ PVHK+YIE+GI +ITCPNVDGYFPSSVKP++TWY G	
Sbjct:	121	YCSKVAFPLEVVQKDSFCNSAMRFPVHKMYIEHGIHKITCPNVDGYFPSSVKPSVTWYKG	180
Query:	843	CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA	1022
		C +I +F+NV+PEGMNLSF I L+SNGNYTCVVTYPENGR FHLTRT+TVKVVGSPK+A	
Sbjct:	181	CTEIVDFHNVLPEGMNLSFFIPLVSNNGNYTCVVTYPENGRFLFHLTRTVTVKVVGSPKDA	240
Query:	1023	VPPVIHSPNDHVVEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE	1202
		+PP I+SPND VVEKEPGEEL+IPC VYFSF+MDS NEVWWTIDGKKPDD+T+D+TINE	
Sbjct:	241	LPPQIYSPNDRVVEKEPGEELVIPCKVYFSFIMDSHNEVWWTIDGKKPDDVTVDITINE	300
Query:	1203	SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVQK	1352
		S+S+S TEDETRTQILSIKKVT EDL+R+YVCHAR+ KGE +AAKVQK	
Sbjct:	301	SVSYSSTEDETRTQILSIKKVTPEDLRRNYVCHARNTKGEAEQAAKVQK	350

FIG.2A

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1 TCTATGAGAAAGAACCAGGAGAGGAGCTACTCATTCCCTGTACGGTCTAT 50
|||||
1060 TCTATGAGAAAGAACCAGGAGAGGAGCTACTCATTCCCTGTACGGTCTAT 1109

51 TTTAGTTTTCTGATGGATTCTCGCAATGAGGTTTGGTGGACCATTGATGG 100
|||||
1110 TTTAGTTTTCTGATGGATTCTCGCAATGAGGTTTGGTGGACCATTGATGG 1159

101 AAAAAAACCTGATGACATCACTATTGATGTCACCATTAAACGAAAGTATAA 150
|||||
1160 AAAAAAACCTGATGACATCACTATTGATGTCACCATTAAACGAAAGTATAA 1209

151 GTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAG 200
|||||
1210 GTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAG 1259

201 AAAGTTACCTCTGAGGATCTCAAGCGCANTANTGTCTGTCATGCTAGAAG 250
|||||: :|||||
1260 AAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAG 1259

251 TGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAG 294
|||||
1310 TGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAG 1353
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FIG.2B

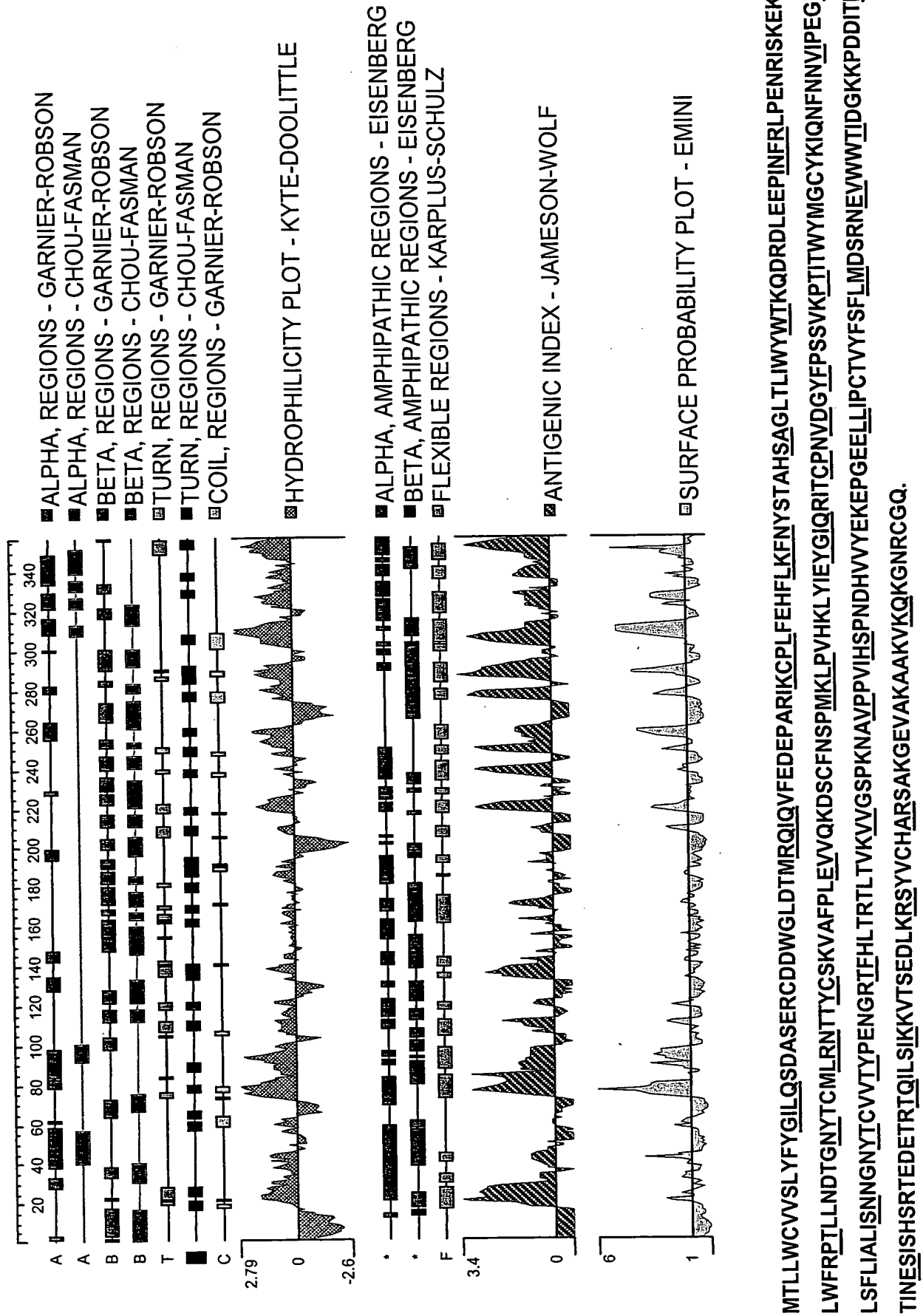


FIG. 3